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wherein said at least one amino acid residue is selected from the group consisting of:

the 11<sup>th</sup> Tyr, 16<sup>th</sup> Glu, 49<sup>th</sup> Asn, 84<sup>th</sup> Glu, 144<sup>th</sup> Ser, 167<sup>th</sup> Gln, 169<sup>th</sup> Tyr, 178<sup>th</sup> Ala, 188<sup>th</sup> Glu, 190<sup>th</sup> Asn, 205<sup>th</sup> His and 209<sup>th</sup> Gln, and

said mutant  $\alpha$  amylase possesses increased heat resistance and maintains resistance to chelating agents when compared to SEQ ID NO:1.

2. (Amended) A mutant  $\alpha$ -amylase obtained by making a' substitution of a sequence corresponding to 11 to 100 amino acid residues from the amino terminus of SEQ ID NO: 1 or by making a substitution of a sequence corresponding to 11 to 100 amino acid residues from the amino terminus of an amino acid sequence having at least 70% home logy to SEQ ID NO: 1,

with another amino acid sequence that encodes a liquefying  $\alpha$ -amylase proteir,

wherein said mutant  $\alpha$ -amylase possesses increased heat resistance and maintains resistance to chelating agents when compared to SEQ ID NO:1.

3. (Amended) The mutant  $\alpha$ -amylase according to Claim 2, wherein an amino terminal sequence from 1<sup>st</sup> Asp through 19<sup>th</sup> Gly

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of SEQ ID NO:1 or an amino terminal sequence corresponding to 1<sup>st</sup> Asp through 19<sup>th</sup> Gly of SEQ ID NO:1 of a sequence having at least 70% homology to SEQ ID NO:1, is substituted with an amino acid sequence encoding another liquefying  $\alpha$ -amylase.

4. (Amended) The mutant  $\alpha$ -amylase according to Claim 2 or 3, wherein said liquefying  $\alpha$ -amylase comprises SEQ ID NO:2.

5. (Amended) A mutant  $\alpha$ -amylase obtained by introducing at least two mutations into SEQ ID NO:1 or an amino acid sequence having at least 70% homology to SEQ ID NO:1,

wherein a first mutation is a substitution or a deletion of at least one amino acid residue selected from the group consisting of the 11<sup>th</sup> Tyr, 16<sup>th</sup> Glu, 49<sup>th</sup> Asn, 84<sup>th</sup> Glu, 144<sup>th</sup> Ser, 167<sup>th</sup> Gln, 169<sup>th</sup> Tyr, 178<sup>th</sup> Ala, 188<sup>th</sup> Glu, 190<sup>th</sup> Asn, 205<sup>th</sup> His and 209<sup>th</sup> Gln, and

wherein a second mutation is a substitution of at least one amino terminal sequence from  $1^{\rm st}$  Asp through  $11^{\rm th}$  Tyr or  $100^{\rm th}$  Asp, and

wherein said mutant  $\alpha$ -amylase possesses increased heat resistance and maintains resistance to chelating agents when compared to SEQ ID NO:1.

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6. (Amended) The mutant  $\alpha$ -amylase according to Claim 5, wherein said first mutation comprises:

the substitution of an amino acid residue selected from the group consisting of: the 11<sup>th</sup> Tyr of SEQ ID NO:1 with Phe, the 16<sup>th</sup> Glu of SEQ ID NO:1 with Pro, the 49<sup>th</sup> Asn of SEQ ID NO:1 with Ser, the 167 Gln of SEQ ID NO:1 with Glu, the 169<sup>th</sup> Tyr of SEQ ID NO:1 with Lys, the 190<sup>th</sup> Asn of SEQ ID NO:1 with Phe, the 205<sup>th</sup> His of SEQ ID NO:1 with Arg, or the 209<sup>th</sup> Gln of SEQ ID NO:1 with Val,

and wherein said second mutation comprises:

substituting an amino terminal sequence from  $1^{\rm st}$  Asp through  $19^{\rm th}$  Gly of SEQ ID NO:1 with an amino acid sequence from  $1^{\rm st}$  His to  $21^{\rm st}$  Gly of SEQ ID NO 2.

Attached hereto is a marked-up version showing the changes made to the application by this Amendment.